

## SEQUENCE LISTING

&lt;110&gt; Unilever plc

Unilever NV

&lt;120&gt; Production of Antibodies

&lt;130&gt; T7060

&lt;160&gt; 67

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; VHH with peptide linker

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(417)

&lt;400&gt; 1

cag	gtg	cag	ctg	cag	gag	tca	ggg	gga	gga	ttg	gtg	cag	gct	ggg	ggc	48
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
1				5					10					15		

tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	ggt	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His	
		20						25					30			

ggt	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt	144
Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg	
		35				40					45					

gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggt	aaa	gag	aca	tgg	tat	aaa	192
Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys	
	50				55					60						

gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	aag	act	240
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Thr	
65					70				75					80		

003727-940000

acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288  
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 85 90 95

tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336  
 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro  
 100 105 110

gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384  
 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser  
 115 120 125

gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa 437  
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 130 135

ttc 440

<210> 2

<211> 139

<212> PRT

<213> Artificial

<400> 2

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His  
 20 25 30

Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg  
 35 40 45

Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys  
 50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr  
 65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro  
 100 105 110

Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser  
 115 120 125

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 130 135

00973746 "131800

```
<220>  
<223>  myc linker  
<400>  3
```

```
<210> 4
<211> 471
<212> DNA
<213> Artificial
```

```
<220>
<223>    VHH with linker
<220>
<221>    CDS
<222>    (1)..(459)
```

<400>																4	
cag	gtg	cag	ctg	cag	cag	tca	ggg	gga	ggc	ttg	gtg	cag	gct	ggg	ggg	48	
Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly		
1				5				10				15					
tct	ctg	aga	ctc	tcc	tgt	gta	gct	tct	gaa	agc	agc	ttc	agc	aac	aat	96	
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Glu	Ser	Ser	Phe	Ser	Asn	Asn		
			20				25				30						
cac	atg	ggc	tgg	tac	cgc	cgg	gct	cca	ggg	aac	cag	cgc	gag	ctg	gtc	144	
His	Met	Gly	Trp	Tyr	Arg	Arg	Ala	Pro	Gly	Asn	Gln	Arg	Glu	Leu	Val		
		35				40				45							
gca	act	att	agt	cct	ggt	ggt	agc	aca	cac	tat	gta	gac	tcc	gtg	aag	192	
Ala	Thr	Ile	Ser	Pro	Gly	Gly	Ser	Thr	His	Tyr	Val	Asp	Ser	Val	Lys		
		50				55				60							
ggc	cga	ttc	acc	atc	tcc	cga	gac	aac	gcc	aag	aac	aca	gtg	tat	cta	240	
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu		
65				70				75				80					
caa	atg	gac	agc	ctg	aaa	cca	gag	gac	acg	gcc	gtc	tat	tac	tgt	gct	288	
Gln	Met	Asp	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala		
				85				90				95					
gcc	aag	ggg	agg	ggg	ctg	cag	gct	atg	cag	tac	tgg	ggc	cag	ggg	acc	336	
Ala	Lys	Gly	Arg	Gly	Leu	Gln	Ala	Met	Gln	Tyr	Trp	Gly	Gln	Gly	Thr		

<210>	5
<211>	153
<212>	PRT
<213>	Artificial

```

<400>      5
Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1              5              10              15
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
      20              25              30
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
      35              40              45
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
      50              55              60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65              70              75              80
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
      85              90              95
Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
      100              105              110
Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
      115              120              125
Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
      130              135              140
Ser Glu Glu Asp Leu Asn Gly Ala Ala
145              150

```

<210> 6  
 <211> 468  
 <212> DNA  
 <213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(456)

<400> 6  
 cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg 48  
 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 1 5 10 15  
 tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata 96  
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile  
 20 25 30  
 gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc 144  
 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val  
 35 40 45  
 gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag 192  
 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu  
 65 70 75 80  
 caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct 288  
 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg 336  
 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc 384  
 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala  
 115 120 125  
 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca 432  
 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser  
 130 135 140  
 gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 468  
 Glu Glu Asp Leu Asn Gly Ala Ala  
 145 150

<210> 7

<211> 152

00947 947260

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 7

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile  
 20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val  
 35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu  
 65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala  
 115 120 125

Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser  
 130 135 140

Glu Glu Asp Leu Asn Gly Ala Ala  
 145 150

&lt;210&gt; 8

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; VHH with linker

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(450)

003626 "944660

<400> 8  
 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48  
 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln  
 1 5 10 15  
  
 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96  
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe  
 20 25 30  
  
 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144  
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg  
 35 40 45  
  
 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192  
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala  
 50 55 60  
  
 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240  
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn  
 65 70 75 80  
  
 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt 288  
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 85 90 95  
  
 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc 336  
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr  
 100 105 110  
  
 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat 384  
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His  
 115 120 125  
  
 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 432  
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu  
 130 135 140  
  
 gat ctg aat ggg gcc gca tagtaacaat tg 462  
 Asp Leu Asn Gly Ala Ala  
 145 150

<210> 9

<211> 150

<212> PRT

<213> Artificial

<400> 9

Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln  
 1 5 10 15  
  
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe  
 20 25 30  
  
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg  
 35 40 45

009722" 92425250

gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240



Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn  
 65 70 75 80  
 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt 288  
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 85 90 95  
 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc 336  
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr  
 100 105 110  
 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat 384  
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His  
 115 120 125  
 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 432  
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu  
 130 135 140  
 gat ctg aat agt gag aaa gat gag cta tgataacaat tg 471  
 Asp Leu Asn Ser Glu Lys Asp Glu Leu  
 145 150  
 <210> 11  
 <211> 153  
 <212> PRT  
 <213> Artificial  
 <400> 11  
 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln  
 1 5 10 15  
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe  
 20 25 30  
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg  
 35 40 45  
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala  
 50 55 60  
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn  
 65 70 75 80  
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val  
 85 90 95  
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr  
 100 105 110  
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His  
 115 120 125

008727 "9246660

His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu  
 130 135 140

Asp Leu Asn Ser Glu Lys Asp Glu Leu  
 145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 12

agctgcgata gcaagcttgg taccgggaat tctctaga

38

<210> 13

<211> 42

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 13

aatttctaga gaattcccg tacciaagctt gcttgcgata gc

42

<210> 14

<211> 31

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 14

tgcacccatg gcccgctagc caattggagc t

31

<210> 15

<211> 23

<212> DNA

009727 92475

<213> Artificial

<220>

<223> synthetic insert

<400> 15

ccaattggct agcgggcat ggg

23

<210> 16

<211> 22

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 16

ccacccacga gggaacatcg tg

22

<210> 17

<211> 39

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 17

gaattcccat ggtttacact cgaggctctc tccaaatga

39

<210> 18

<211> 189

<212> DNA

<213> Artificial

<220>

<223> PCR product

<400> 18

ccacccacga gggaacatcg tggaaaaaga agacgttcca accacgtctt caaagcaagt 60

ggattgatgt gatattcca ctgacgtaag ggatgacgca caatcccact atccttcgca 120

agacccttcc tttatataag gaagttcatt tcatttggag aggacctcga gtgtaaacca 180

00877 324660

tggaattc

189

<210> 19

<211> 21

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 19

ccggcaacag gattcaatct t

21

<210> 20

<211> 40

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 20

agctccatgg gatttgttct cttttcaciaa ttgccttcat

40

<210> 21

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 21

ttcttcttgt ctctacactt ctcttattcc tagta

35

<210> 22

<211> 35

<212> DNA

<213> Artificial

003721 "947660



Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln Val  
20 25 30

Gln Leu

&lt;210&gt; 29

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 29

gacatcccat ggcaagcatc a

21

&lt;210&gt; 30

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 30

aagcttggtta acagccctta a

21

&lt;210&gt; 31

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 31

agggttggtta acaaacttga t

21

&lt;210&gt; 32

&lt;211&gt; 44

&lt;212&gt; DNA

&lt;213&gt; Artificial

008747 "92426260

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 32

agactgctgc agctgcacct gctttccaca aacaatggta gctg

44

&lt;210&gt; 33

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; sequencing primer

&lt;400&gt; 33

aattaaccct cactaaagg

19

&lt;210&gt; 34

&lt;211&gt; 254

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; GBSS leader

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(254)

&lt;400&gt; 34

cc atg gca agc atc aca gct tca cac cac ttt gtg tca aga agc caa  
 Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln  
 1 5 10 15

47

act tca cta gac acc aaa tca acc ttg tca cag ata gga ctc agg aac  
 Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn  
 20 25 30

95

cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg  
 His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly  
 35 40 45

143

ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga  
 Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg  
 50 55 60

191

act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa  
 Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys  
 65 70 75

239

008727 " 92426.468



254

<210> 35

<211> 84

<212> PRT

<213> Artificial

<400> 35

Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln Thr  
1 5 10 15

Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn His  
20 25 30

Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly Leu  
35 40 45

Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg Thr  
50 55 60

Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys Gln  
65 70 75 80

Val Gln Leu Gln

<210> 36

<211> 18

<212> DNA

<213> Artificial

 $\langle 220 \rangle$ 

<223> synthetic insert

<400> 36

18

<210> 37

<211> 10

<212> DNA

<213> Artificial

&lt;220&gt;

&lt;223&gt; synthetic insert

<400> 37  
gctgcacctg

10

&lt;210&gt; 38

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; PCR primer

<400> 38  
cgcaagaccc ttcctctata taag

24

&lt;210&gt; 39

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; PCR primer

<400> 39  
gagctcgaat tcttattata gctcatcttt ctctgaattc agatcctctt ctgagatgag

60

&lt;210&gt; 40

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; linker

&lt;400&gt; 40

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr.  
20 25

008737 324260

<210> 41

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 41  
atcctcaact tccaatcaga

20

<210> 42

<211> 19

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 42  
ttcttgagag atagcttga

19

<210> 43

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 43  
gatcccatgg cccgctagcc aattggagct

30

<210> 44

<211> 22

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 44  
ccaattggct agcgggccat gg

22

<210> 45

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 45  
gatccacctc gagtgtaaac catggcccg

29

<210> 46

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 46  
ctagcgggcc atggtttaca ctcgaggtg

29

<210> 47

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 47  
attgcctacg gcagccgctg

20

<210> 48

<211> 51

<212> DNA

<213> Artificial

008727 924260

<220>

<223> PCR primer

<400> 48

tccaaccaat tggtactatg cggccccatt cagatcctct tctgagatga g

51

<210> 49

<211> 25

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 49

gtctgtctaa agtaaagtag atgcg

25

<210> 50

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 50

tccaaccaat tggtatcata gtcactcttt ctactattc agatcctctt ctgagatgag

60

<210> 51

<211> 29

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 51

agtccccat ggtacgtcct gtagaaacc

29

<210> 52

<211> 25

<212> DNA

005722 9242260

<213> Artificial

<220>

<223> PCR primer

<400> 52

cgttttcgtc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53

cgcaagaccc ttcttttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct  
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala  
1 5 10 15

47

ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt  
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser  
20 25 30

95

ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag  
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys  
35 40 45

143

gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg  
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp  
50 55 60

191

<213> Artificial

<220>

<223> PCR primer

<400> 52  
cgttttcgtc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53  
cgcaagacc ttcctttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54  
cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct 47  
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala  
1 5 10 15  
ggg ggc tct ctg aga ctc tcc tgt gca gcc tog gga cgc gcc acc agt 95  
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser  
20 25 30  
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag 143  
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys  
35 40 45  
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg 191  
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp  
50 55 60

008746 9474660

tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala 65 70 75	239
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr 80 85 90 95	287
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser 100 105 110	335
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val 115 120 125	383
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca caa Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln 130 135 140	431
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala 145 150 155	479
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro 160 165 170 175	527
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val 180 185 190	575
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile 195 200 205	623
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911
gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly 305 310 315	959
acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe 320 325 330 335	1007

0093743 12300 92426260



ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055  
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu  
                   340                  345                  350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103  
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr  
                   355                  360                  365

cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa 1154  
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys  
                   370                  375

<210> 55

<211> 377

<212> PRT

<213> Artificial

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly  
 1                  5                  10                  15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly  
                   20                  25                  30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu  
                   35                  40                  45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr  
                   50                  55                  60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys  
 65                  70                  75                  80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala  
                   85                  90                  95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu  
                   100                  105                  110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser  
                   115                  120                  125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro  
                   130                  135                  140

Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro  
 145                  150                  155                  160

Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys  
                   165                  170                  175

008727" 9242E260

Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val  
 180 185 190

Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp  
 195 200 205

Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe  
 210 215 220

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp  
 225 230 235 240

Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu  
 245 250 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg  
 260 265 270

Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys  
 275 280 285

Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp  
 290 295 300

Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr  
 305 310 315 320

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu  
 325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr  
 340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys  
 370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

003461330

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(1154)

&lt;400&gt; 56

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct	47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala	
1 5 10 15	
ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt	95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser	
20 25 30	
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag	143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys	
35 40 45	
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg	191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp	
50 55 60	
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc	239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	
65 70 75	
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg	287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr	
80 85 90 95	
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc	335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser	
100 105 110	
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc	383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val	
115 120 125	
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca cca	431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln	
130 135 140	
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc	479
Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala	
145 150 155	
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc	527
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro	
160 165 170 175	
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg	575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val	
180 185 190	
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att	623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile	
195 200 205	
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag	671
Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln	
210 215 220	
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag	719
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln	
225 230 235	

09737476 "121800

gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct 767  
 Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala  
 240 245 250 255

ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc 815  
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr  
 260 265 270

cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc 863  
 Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala  
 275 280 285

aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct 911  
 Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro  
 290 295 300

gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc 959  
 Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly  
 305 310 315

acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc 1007  
 Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe  
 320 325 330 335

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055  
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu  
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103  
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr  
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa tct gag aaa gat gag cta 1151  
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu  
 370 375 380

taa taagaattcg agctcgaa 1172

&lt;210&gt; 57

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 57

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly  
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly  
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu  
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr  
 50 55 60

09737476 131300





<211> 42

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 61

ttcgagctcg aattcttatt atttaccga agactgggtg at

42

<210> 62

<211> 27

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 62

ctgaggagac ggtgacctgg gtccct

27

<210> 63

<211> 46

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 63

agcccctgag ctctgtggag ggccctcagt cttcatcttc cccccg

46

<210> 64

<211> 61

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 64

ttcgagctcg aattcttatt atttaccga agactgggtg atggatttct ggggtgtagtg

60

008727 924260

g

61

&lt;210&gt; 65

&lt;211&gt; 79

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 65

ttcgagctcg aattcttatt atagctcatc tttctcagat ttacccgaag actgggtgat 60

ggatttctgg gtgtagtg 79

&lt;210&gt; 66

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; VHH with linker

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(449)

&lt;400&gt; 66

cc atg gcc cag gtg cag ctg cag gag tct ggg gga ggc ttg gtg cag 47  
 Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln  
 1 5 10 15

gct ggg ggg tct ctg agg ctc tcc tgt gca gcc tct gga agc att ttc 95  
 Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe  
 20 25 30

aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc 143  
 Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg  
 35 40 45

gag ttg gtc gca ctg att tct gcg ggt ggt cgt aca tgg tat gca gac 191  
 Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp  
 50 55 60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg 239  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr  
 65 70 75

ctg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat 287

00346 1300 924260



Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr  
80 85 90 95

tac tgt act gcc ggg ggt tcg tac tgg ggc cag ggg acc cag gtc acc 335  
Tyr Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr  
100 105 110

gtc gcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc gcc cat 383  
Val Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His  
115 120 125

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 431  
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu  
130 135 140

gat ctg aat ggg gcc gca tagtaacaat tg 461  
Asp Leu Asn Gly Ala Ala  
145

<210> 67

<211> 149

<212> PRT

<213> Artificial

<400> 67

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala  
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Arg  
20 25 30

Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg Glu  
35 40 45

Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp Ser  
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu  
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr  
85 90 95

Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val  
100 105 110

Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His His  
115 120 125

His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp  
130 135 140

008467 9246260

Leu Asn Gly Ala Ala  
145

09737475 121800

United States Patent & Trademark Office  
Office of Initial Patent Examination

Application papers not suitable for publication

SN 09-137-476 Mail Date 12-18-00

- ☐ Non-English Specification
- ☒ Specification contains drawing(s) on page(s) \_\_\_\_\_ or table(s) 57-59
- ☐ Landscape orientation of text ☐ Specification ☐ Claims ☐ Abstract
- ☐ Handwritten ☐ Specification ☐ Claims ☐ Abstract
- ☐ More than one column ☐ Specification ☐ Claims ☐ Abstract
- ☐ Improper line spacing ☐ Specification ☐ Claims ☐ Abstract
- ☐ Claims not on separate page(s)
- ☐ Abstract not on separate page(s)
- ☐ Improper paper size -- Must be either A4 (21 cm x 29.7 cm) or 8-1/2"x 11"
- ☐ Specification page(s) \_\_\_\_\_ ☐ Abstract
- ☐ Drawing page(s) \_\_\_\_\_ ☐ Claim(s)
- ☐ Improper margins
- ☐ Specification page(s) \_\_\_\_\_ ☐ Abstract
- ☐ Drawing page(s) \_\_\_\_\_ ☐ Claim(s)
- ☐ Not reproducible
- | <u>Reason</u>                                 | <u>Section</u>                                       |
|---|--|
| <input type="checkbox"/> Paper too thin       | <input type="checkbox"/> Specification page(s) _____ |
| <input type="checkbox"/> Glossy pages         | <input type="checkbox"/> Drawing page(s) _____       |
| <input type="checkbox"/> Non-white background | <input type="checkbox"/> Abstract                    |
|   | <input type="checkbox"/> Claim(s)                    |
- ☐ Drawing objection(s)
- ☐ Missing lead lines, drawing(s) \_\_\_\_\_
- ☐ Line quality is too light, drawing(s) \_\_\_\_\_
- ☐ More than 1 drawing and not numbered correctly
- ☐ Non-English text, drawing(s) \_\_\_\_\_
- ☐ Excessive text, drawing(s) \_\_\_\_\_
- ☐ Photographs capable of illustration, drawing(s) \_\_\_\_\_

008700 944260

United States Patent & Trademark Office  
Office of Initial Patent Examination -- Scanning Division



Application deficiencies found during scanning:

☐ Page(s) \_\_\_\_\_ of \_\_\_\_\_ were not present  
for scanning. (Document title)

☐ Page(s) \_\_\_\_\_ of \_\_\_\_\_ were not present  
for scanning. (Document title)

☐ *Scanned copy is best available.*

File 6 6126 23 sheets of drawing